

RAW SEQUENCE LISTING

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Application Serial Number: 10/569,791
Source: IFWO
Date Processed by STIC: 12/05/2006

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DATE: 12/05/2006

PATENT APPLICATION: US/10/569,791

TIME: 12:30:38

Input Set : N:\efs\12_05_06\10569791_efs\2006112012540305PUS1.txt

Output Set: N:\CRF4\12052006\J569791.raw

3 <110> APPLICANT: Yorimasa SUWA et al.
 5 <120> TITLE OF INVENTION: TARGET PROTEIN OF ANTIDIABETIC AND NOVEL ANTIDIABETIC
 "INSUFUL"

7 <130> FILE REFERENCE: 1254-0305PUS1

9 <140> CURRENT APPLICATION NUMBER: 10/569,791

10 <141> CURRENT FILING DATE: 2006-02-27

12 <150> PRIOR APPLICATION NUMBER: PCT/JP04/16996

13 <151> PRIOR FILING DATE: 2004-11-16

15 <150> PRIOR APPLICATION NUMBER: JP 2003/402164

16 <151> PRIOR FILING DATE: 2003-12-01

18 <160> NUMBER OF SEQ ID NOS: 3

20 <170> SOFTWARE: PatentIn Ver. 2.0

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 2617

24 <212> TYPE: DNA

25 <213> ORGANISM: Homo sapiens

27 <400> SEQUENCE: 1

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30 ggggtgattc ggcacaaacc gcccgaccca ggggccggtg cgcgtgtgga aggggaagca 180
31 ctccccctgt ggtcgcctgg aggtgcgctg gaggagggg tgacataacc agggactcga 240
32 ggtccgccgt gggaatgac cagcaactgc tcttggtctt gagcgggtac cctgggtcca 300
33 ttttcacctg gaacaagcgg agtgccctgc aggtatcgca ggacttccct ttcctccacc 360
34 ccagtggagc cagtgtcctg aatcgactct gccggctcgg cacagactat attcgcttca 420
35 ctgagttcat tgaacagtac acggggccatg tgcaacagca ggatcaccat ccattctcaac 480
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57 gggccctaca aatgcagcgc aagcacctca agtcgaacca gactgatgca atcaagtggc 1800
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67 cacaaataaa tatctgcggc ttagtgatag gactctacct tttctcctag aagcagttac 2400
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73 <210> SEQ ID NO: 2

74 <211> LENGTH: 657

75 <212> TYPE: PRT

76 <213> ORGANISM: Homo sapiens

78 <400> SEQUENCE: 2

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82 Phe Thr Trp Asn Lys Arg Ser Gly Leu Gln Val Ser Gln Asp Phe Pro
83 20 25 30
85 Phe Leu His Pro Ser Glu Thr Ser Val Leu Asn Arg Leu Cys Arg Leu
86 35 40 45
88 Gly Thr Asp Tyr Ile Arg Phe Thr Glu Phe Ile Glu Gln Tyr Thr Gly
89 50 55 60
91 His Val Gln Gln Gln Asp His His Pro Ser Gln Gln Gly Gln Gly Gly
92 65 70 75 80
94 Leu His Gly Ile Tyr Leu Arg Ala Phe Cys Thr Gly Leu Asp Ser Val
95 85 90 95
97 Leu Gln Pro Tyr Arg Gln Ala Leu Leu Asp Leu Glu Gln Glu Phe Leu
98 100 105 110
100 Gly Asp Pro His Leu Ser Ile Ser His Val Asn Tyr Phe Leu Asp Gln
101 115 120 125
103 Phe Gln Leu Leu Phe Pro Ser Val Met Val Val Val Glu Gln Ile Lys
104 130 135 140
106 Ser Gln Lys Ile His Gly Cys Gln Ile Leu Glu Thr Val Tyr Lys His
107 145 150 155 160
109 Ser Cys Gly Gly Leu Pro Pro Val Arg Ser Ala Leu Glu Lys Ile Leu
110 165 170 175
112 Ala Val Cys His Gly Val Met Tyr Lys Gln Leu Ser Ala Trp Met Leu
113 180 185 190
115 His Gly Leu Leu Leu Asp Gln His Glu Glu Phe Phe Ile Lys Gln Gly
116 195 200 205
118 Pro Ser Ser Gly Asn Val Ser Ala Gln Pro Glu Glu Asp Glu Glu Asp

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119      210      215      220
121 Leu Gly Ile Gly Gly Leu Thr Gly Lys Gln Leu Arg Glu Leu Gln Asp
122 225      230      235      240
124 Leu Arg Leu Ile Glu Glu Glu Asn Met Leu Ala Pro Ser Leu Lys Gln
125      245      250      255
127 Phe Ser Leu Arg Val Glu Ile Leu Pro Ser Tyr Ile Pro Val Arg Val
128      260      265      270
130 Ala Glu Lys Ile Leu Phe Val Gly Glu Ser Val Gln Met Phe Glu Asn
131      275      280      285
133 Gln Asn Val Asn Leu Thr Arg Lys Gly Ser Ile Leu Lys Asn Gln Glu
134      290      295      300
136 Asp Thr Phe Ala Ala Glu Leu His Arg Leu Lys Gln Gln Pro Leu Phe
137 305      310      315      320
139 Ser Leu Val Asp Phe Glu Gln Val Val Asp Arg Ile Arg Ser Thr Val
140      325      330      335
142 Ala Glu His Leu Trp Lys Leu Met Val Glu Glu Ser Asp Leu Leu Gly
143      340      345      350
145 Gln Leu Lys Ile Ile Lys Asp Phe Tyr Leu Leu Gly Arg Gly Glu Leu
146      355      360      365
148 Phe Gln Ala Phe Ile Asp Thr Ala Gln His Met Leu Lys Thr Pro Pro
149      370      375      380
151 Thr Ala Val Thr Glu His Asp Val Asn Val Ala Phe Gln Gln Ser Ala
152 385      390      395      400
154 His Lys Val Leu Leu Asp Asp Asp Asn Leu Leu Pro Leu Leu His Leu
155      405      410      415
157 Thr Ile Glu Tyr His Gly Lys Glu His Lys Ala Asp Ala Thr Gln Ala
158      420      425      430
160 Arg Glu Gly Pro Ser Arg Glu Thr Ser Pro Arg Glu Ala Pro Ala Ser
161      435      440      445
163 Gly Trp Ala Ala Leu Gly Leu Ser Tyr Lys Val Gln Trp Pro Leu His
164      450      455      460
166 Ile Leu Phe Thr Pro Ala Val Leu Glu Lys Tyr Asn Val Val Phe Lys
167 465      470      475      480
169 Tyr Leu Leu Ser Val Arg Arg Val Gln Ala Glu Leu Gln His Cys Trp
170      485      490      495
172 Ala Leu Gln Met Gln Arg Lys His Leu Lys Ser Asn Gln Thr Asp Ala
173      500      505      510
175 Ile Lys Trp Arg Leu Arg Asn His Met Ala Phe Leu Val Asp Asn Leu
176      515      520      525
178 Gln Tyr Tyr Leu Gln Val Asp Val Leu Glu Ser Gln Phe Ser Gln Leu
179      530      535      540
181 Leu His Gln Ile Asn Ser Thr Arg Asp Phe Glu Ser Ile Arg Leu Ala
182 545      550      555      560
184 His Asp His Phe Leu Ser Asn Leu Leu Ala Gln Ser Phe Ile Leu Leu
185      565      570      575
187 Lys Pro Val Phe His Cys Leu Asn Glu Ile Leu Asp Leu Cys His Ser
188      580      585      590
190 Phe Cys Ser Leu Val Ser Gln Asn Leu Gly Pro Leu Asp Glu Arg Gly
191      595      600      605

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197 625                      630                      635                      640
199 Asp Leu Ala Gln Leu Leu Leu Arg Leu Asp Tyr Asn Lys Tyr Tyr Thr
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203      660                      665
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 667
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 3
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217 Phe Thr Trp Asn Lys Arg Ser Gly Leu Gln Val Ser Gln Asp Phe Pro
218      20                      25                      30
221 Phe Leu His Pro Ser Glu Thr Ser Val Leu Asn Arg Leu Cys Arg Leu
222      35                      40                      45
225 Gly Thr Asp Tyr Ile Arg Phe Thr Glu Phe Ile Glu Gln Tyr Thr Gly
226      50                      55                      60
229 His Val Gln Gln Gln Asp His His Pro Ser Gln Gln Gly Gln Gly Gly
230 65                      70                      75                      80
233 Leu His Gly Ile Tyr Leu Arg Ala Phe Cys Thr Gly Leu Asp Ser Val
234      85                      90                      95
237 Leu Gln Pro Tyr Arg Gln Ala Leu Leu Asp Leu Glu Gln Glu Phe Leu
238      100                     105                     110
241 Gly Asp Pro His Leu Ser Ile Ser His Val Asn Tyr Phe Leu Asp Gln
242      115                     120                     125
245 Phe Gln Leu Leu Phe Pro Ser Val Met Val Val Val Glu Gln Ile Lys
246      130                     135                     140
249 Ser Gln Lys Ile His Gly Cys Gln Ile Leu Glu Thr Val Tyr Lys His
250 145                     150                     155                     160
253 Ser Cys Gly Gly Leu Pro Pro Val Arg Ser Ala Leu Glu Lys Ile Leu
254      165                     170                     175
257 Ala Val Cys His Gly Val Met Tyr Lys Gln Leu Ser Ala Trp Met Leu
258      180                     185                     190
261 His Gly Leu Leu Leu Asp Gln His Glu Glu Phe Phe Ile Lys Gln Gly
262      195                     200                     205
265 Pro Ser Ser Gly Asn Val Ser Ala Gln Pro Glu Glu Asp Glu Glu Asp
266      210                     215                     220
269 Leu Gly Ile Gly Gly Leu Thr Gly Lys Gln Leu Arg Glu Leu Gln Asp
270 225                     230                     235                     240
273 Leu Arg Leu Ile Glu Glu Asn Met Leu Ala Pro Ser Leu Lys Gln
274      245                     250                     255
277 Phe Ser Leu Arg Val Glu Ile Leu Pro Ser Tyr Ile Pro Val Arg Val
278      260                     265                     270
281 Ala Glu Lys Ile Leu Phe Val Gly Glu Ser Val Gln Met Phe Glu Asn
282      275                     280                     285

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285 Gln Asn Val Asn Leu Thr Arg Lys Gly Ser Ile Leu Lys Asn Gln Glu
286      290      295      300
289 Asp Thr Phe Ala Ala Glu Leu His Arg Leu Lys Gln Gln Pro Leu Phe
290 305      310      315      320
293 Ser Leu Val Asp Phe Glu Gln Val Val Asp Arg Ile Arg Ser Thr Val
294      325      330      335
297 Ala Glu His Leu Trp Lys Leu Met Val Glu Glu Ser Asp Leu Leu Gly
298      340      345      350
301 Gln Leu Lys Ile Ile Lys Asp Phe Tyr Leu Leu Gly Arg Gly Glu Leu
302      355      360      365
305 Phe Gln Ala Phe Ile Asp Thr Ala Gln His Met Leu Lys Thr Pro Pro
306      370      375      380
309 Thr Ala Val Thr Glu His Asp Val Asn Val Ala Phe Gln Gln Ser Ala
310 385      390      395      400
313 His Lys Val Leu Leu Asp Asp Asp Asn Leu Leu Pro Leu Leu His Leu
314      405      410      415
317 Thr Ile Glu Tyr His Gly Lys Glu His Lys Ala Asp Ala Thr Gln Ala
318      420      425      430
321 Arg Glu Gly Pro Ser Arg Glu Thr Ser Pro Arg Glu Ala Pro Ala Ser
322      435      440      445
325 Gly Trp Ala Ala Leu Gly Leu Ser Tyr Lys Val Gln Trp Pro Leu His
326      450      455      460
329 Ile Leu Phe Thr Pro Ala Val Leu Glu Lys Tyr Asn Val Val Phe Lys
330 465      470      475      480
333 Tyr Leu Leu Ser Val Arg Arg Val Gln Ala Glu Leu Gln His Cys Trp
334      485      490      495
337 Ala Leu Gln Met Gln Arg Lys His Leu Lys Ser Asn Gln Thr Asp Ala
338      500      505      510
341 Ile Lys Trp Arg Leu Arg Asn His Met Ala Phe Leu Val Asp Asn Leu
342      515      520      525
345 Gln Tyr Tyr Leu Gln Val Asp Val Leu Glu Ser Gln Phe Ser Gln Leu
346      530      535      540
349 Leu His Gln Ile Asn Ser Thr Arg Asp Phe Glu Ser Ile Arg Leu Ala
350 545      550      555      560
353 His Asp His Phe Leu Ser Asn Leu Leu Ala Gln Ser Phe Ile Leu Leu
354      565      570      575
357 Lys Pro Val Phe His Cys Leu Asn Glu Ile Leu Asp Leu Cys His Ser
358      580      585      590
361 Phe Cys Ser Leu Val Ser Gln Asn Leu Gly Pro Leu Asp Glu Arg Gly
362      595      600      605
365 Ala Ala Gln Leu Ser Ile Leu Val Lys Gly Phe Ser Arg Gln Ser Ser
366      610      615      620
369 Leu Leu Phe Lys Ile Leu Ser Ser Val Arg Asn His Gln Ile Asn Ser
370 625      630      635      640
373 Asp Leu Ala Gln Leu Leu Leu Arg Leu Asp Tyr Asn Lys Tyr Tyr Thr
374      645      650      655
377 Gln Ala Gly Gly Thr Leu Gly Ser Phe Gly Met
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VERIFICATION SUMMARY

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